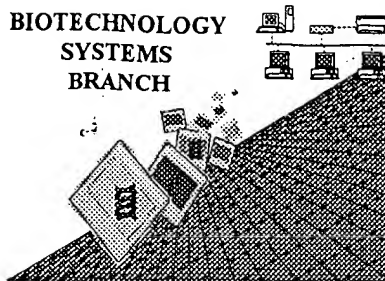


## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/830,111

Source: Pct/09

Date Processed by STIC: 8/30/2001

54  
#6

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

| ERROR DETECTED   | SUGGESTED CORRECTION  | SERIAL NUMBER: 09/830,111 |
|--|---|---------------------------|
| ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE |   |                           |
| 1 <u>Wrapped Nucleics<br/>Wrapped Aminos</u>   | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."  |                           |
| 2 <u>Invalid Line Length</u>   | The rules require that a line not exceed 72 characters in length. This includes white spaces.   |                           |
| 3 <u>Misaligned Amino<br/>Numbering</u>  | The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.   |                           |
| 4 <u>Non-ASCII</u>   | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.  |                           |
| 5 <u>Variable Length</u>   | Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.  |                           |
| 6 <u>PatentIn 2.0<br/>"bug"</u>  | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.   |                           |
| 7 <u>Skipped Sequences<br/>(OLD RULES)</u>   | Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:<br>(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)<br>(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)<br>(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)<br>This sequence is intentionally skipped<br><br>Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. |                           |
| 8 <u>Skipped Sequences<br/>(NEW RULES)</u>   | Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.<br><210> sequence id number<br><400> sequence id number<br>000  |                           |
| 9 <u>Use of n's or Xaa's<br/>(NEW RULES)</u>   | Use of n's and/or Xaa's have been detected in the Sequence Listing.<br>Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.<br>In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.  |                           |
| 10 <u>Invalid &lt;213&gt;<br/>Response</u>   | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence   |                           |
| 11 <u>Use of &lt;220&gt;</u>   | Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.<br>Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.<br>(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)   |                           |
| 12 <u>PatentIn 2.0<br/>"bug"</u>   | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.   |                           |
| 13 <u>Misuse of n</u>  | n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.   |                           |

PCT09

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/830,111

DATE: 08/30/2001  
TIME: 11:37:14

Input Set : A:\ES.txt  
Output Set: N:\CRF3\08302001\I830111.raw

Does Not Comply  
Corrected Diskette Needed

OK → 3 <110> APPLICANT: Kaneka Corporation  
5 <120> TITLE OF INVENTION: Process for producing coenzyme Q10  
7 <130> FILE REFERENCE: T549/QX-GT2  
8 <140> CURRENT APPLICATION NUMBER: US/09/830,111  
8 <141> CURRENT FILING DATE: 2001-07-23  
8 <150> PRIOR APPLICATION NUMBER: JP P1999-237561  
9 <151> PRIOR FILING DATE: 1999-08-24  
W--> 10 <160> NUMBER OF SEQ ID: 2

## ERRORED SEQUENCES

W--> 11 <210> SEQ ID NO: 1  
12 <211> LENGTH: 1653  
13 <212> TYPE: DNA  
14 <213> ORGANISM: *Saioella complicata*  
W--> 15 <400> SEQUENCE: 1  
E--> 17 20 ttttgtgggg tcgaaaagtc ggcacgggtg caggttcggc ttgagaccag taaaggctcg 60  
19 gagattgagt tcaggacaaa gctttgatcc gtgaggtcta catcttcagc aaatcatttc 120  
21 aaatccatat acc atg gcc tca cca gca ctg cgg ata cga agc atc agc 169  
W--> 23 25 Met Ala Ser Pro Ala Leu Arg Ile Arg Ser Ile Ser  
W--> 25 1 5 10  
E--> 28 2  
30 tct cga tca atc gcc tct ctg cga tcg gtt acc cta aga aca gcc tcg 217  
31 Ser Arg Ser Ile Ala Ser Leu Arg Ser Val Thr Leu Arg Thr Ala Ser  
W--> 32 20 25  
E--> 33 5  
E--> 34 gca cct tca tta cga cta aga tgt acc cog acg ago cgg cca tcg agt 265  
35 Ala Pro Ser Leu Arg Leu Arg Cys Thr Pro Thr Ser Arg Pro Ser Ser  
W--> 36 30 35 40  
E--> 38 10 tca tgg get get get gtg tct tcg gcg tcg aga ctg gtt gag cct gat 313  
W--> 39 Ser Trp Ala Ala Ala Val Ser Ser Ala Ser Arg Leu Val Glu Pro Asp  
W--> 40 45 50 55 60  
42 ccg aat caa cct ctc atc aat ccg ctc aac ttg gtc ggt ccc gag atg 361  
W--> 43 15 Pro Asn Gln Pro Leu Ile Asn Pro Leu Asn Leu Val Gly Pro Glu Met  
W--> 44 65 70 75  
45 tca aat ctt aca tcc aac atc cga tct ctc ctc ggt tca gga cac cct 409  
46 Ser Asn Leu Thr Ser Asn Ile Arg Ser Leu Leu Gly Ser Gly His Pro  
W--> 47 20 80 85 90  
E--> 49 tct ctc gac act gtc get aaa tac tat gtt cag tct gag gga aag cat 457  
50 Ser Leu Asp Thr Val Ala Lys Tyr Tyr Val Gln Ser Glu Gly Lys His  
W--> 51 95 100 105  
E--> 52 25  
E--> 53 att cgt cog ctc atg gta ctg ctg atg get cag gcg acg gag gtt gcg 505  
E--> 57 3  
59 Ile Arg Pro Leu Met Val Leu Leu Met Ala Gln Ala Thr Glu Val Ala  
W--> 60 110 115 120

*see following pages  
for explanation -*

*many  
errors*

*Please  
consult  
sequence  
Rules  
for valid  
format*

09/830,111 2

~~Sequence listing~~

<110> Kaneka Corporation

(5) <120> Process for producing coenzyme Q10

<130> T549/QX-GT2

<150> JP P1999-237561

<151> 1999-08-24

<160> 2

<210> 1

<211> 1653

<212> DNA

<213> Saioella complicata

<400> 1

(20) ttttgtgggg tcgaaaagtc ggcacgggtg caggttcggc ttgagaccag taaaggctcg 60

gagattgagt tcaggacaaa gctttgatcc gtgaggtcta catcttcagc aaatcatttc 120

aaatccatat acc atg gcc tca cca gca ctg cgg ata cga agc atc agc 169

(25) Met Ala Ser Pro Ala Leu Arg Ile Arg Ser Ile Ser

DO NOT use TAB codes.  
amino acids MUST be  
directly under  
respective  
codons.

1 5 10

misaligned nos. - see item 3  
on Enr form may  
that

(2)

tct cga tca atc gcc tct ctg cga tcg gtt acc cta aga aca gcc tcg 217  
Ser Arg Ser Ile Ala Ser Leu Arg Ser Val Thr Leu Arg Thr Ala Ser

misaligned

20

25

invalid nucleic acid designator

gca cct tca tta cga cta aga tgt acc cgg acg agc cgg cca tcg agt 265  
Ala Pro Ser Leu Arg Leu Arg Cys Thr Pro Thr Ser Arg Pro Ser Ser

30

35

40

(10) tca tgg get get get invalid tct tcg gcg tcg aga ctg gtt gag cct gat 313  
Ser Trp Ala Ala Ala Val Ser Ser Ala Ser Arg Leu Val Glu Pro Asp  
45 50 55 60

ccg aat caa cct ctc atc aat ccg ctc aac ttg gtc ggt ccc gag atg 361  
Pro Asn Gln Pro Leu Ile Asn Pro Leu Asn Leu Val Gly Pro Glu Met  
65 70 75

(20) tca aat ctt aca tcc aac atc cga tct ctc ctc ggt tca gga cac cct 409  
Ser Asn Leu Thr Ser Asn Ile Arg Ser Leu Leu Gly Ser Gly His Pro  
80 85 90

tct ctc gac act gtc get invalid aaa tac tat gtt cag tct gag gga aag cat 457  
Ser Leu Asp Thr Val Ala Lys Tyr Tyr Val Gln Ser Glu Gly Lys His  
95 100 105

(25) att cgt cor ctc atg gta ctg ctg atg get invalid cag gcg acg gag gtt gcg 505  
invalid invalid

(3)

delete  
ALL  
line  
numbers

09/830,111 3

Ile Arg Pro Leu Met Val Leu Leu Met Ala Gln Ala Thr Glu Val Ala

110 115 120

*misaligned*

cca aaa gtt cag ggt tgg gag aag gtc gtg gag gtt ccg gtg aac gag 553  
Pro Lys Val Gln Gly Trp Glu Lys Val Val Glu Val Pro Val Asn Glu  
125 130 135 140

gga ctc gca cca cca gag gtg ctc aat gac aag aac cca gat atg atg 601  
Gly Leu Ala Pro Pro Glu Val Leu Asn Asp Lys Asn Pro Asp Met Met

145 150 155

aac atg agg tca gga cca tta acg aag gac ggc gag atc gag gga cag 649  
Asn Met Arg Ser Gly Pro Leu Thr Lys Asp Gly Glu Ile Glu Gly Gln

160 165 170

acg tcg aat atc ctc gcc tcg caa cgg cgg ttg get gag atc acg gag 697  
Thr Ser Asn Ile Leu Ala Ser Gln Arg Arg Leu Ala Glu Ile Thr Glu  
175 180 185

atg atc cat gca gca tca ctc ctc cac gac gac gtt atc gac get tcc 745  
Met Ile His Ala Ala Ser Leu Leu His Asp Asp Val Ile Asp Ala Ser  
190 195 200

*invalid*

gag acc aga cga aac gca cca tcc gga aac cag gca ttc gga aac aag 793  
Glu Thr Arg Arg Am Ala Pro Ser Gly Asn Gln Ala Phe Gly Asn Lys

205 210 215 220

4

atg gcg att ttg get ggt gat ttc ttg ttg gga cgg gcg tct gtt gca 841  
Met Ala Ile Leu Ala Gly Asp Phe Leu Leu Gly Arg Ala Ser Val Ala

225 230 235

ttg gcg agg ttg cgc aat ccg gag gtg att gag ctt ttg get act gtt 889  
Leu Ala Arg Leu Arg Asn Pro Glu Val Ile Glu Leu Leu Ala Thr Val

240 245 250

att gca aac ttg gtt gag gga gag ttc atg cag ttg aaa aat act gtt 937  
Ile Ala Asn Leu Val Glu Gly Glu Phe Met Gln Leu Lys Asn Thr Val

255 260 265

gat gat gcg att gag get acg gcg acg cag gaa acg ttc gat tac tat 985  
Asp Asp Ala Ile Glu Ala Thr Ala Thr Gln Glu Thr Phe Asp Tyr Tyr

270 275 280

ttg cag aag act tac ttg aag act gcg tcc ttg att gcc aag tcg tgc 1033  
Leu Gln Lys Thr Tyr Leu Lys Thr Ala Ser Leu Ile Ala Lys Ser Cys

285 290 295 300

aga gca agt gcg ctt get ggt ggt get acg get gag gtt get gat get 1081  
Arg Ala Ser Ala Leu Leu Gly Gly Ala Thr Pro Glu Val Ala Asp Ala

305 310 315

get tat get tac gga agg aac ctt ggt ttg gca ttc cag atc gtc gac 1129

*move amino acids directly under codons*

5

Ala Tyr Ala Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Ile Val Asp  
 320 325 330 *misaligned*

gac atg ctc gac tac acc gtc tcc ggt acc gac ctc ggt aag ccc gcc 1177  
 5 ← Asp Met Leu Asp Tyr Thr Val Ser Ala Thr Asp Leu Gly Lys Pro Ala  
*move over* 335 340 345

ggt gca gac ctc cag ctc ggt ctc gcc acc gcg ccg gcc ctc ttc gca 1225  
 Gly Ala Asp Leu Gln Leu Gly Leu Ala Thr Ala Pro Ala Leu Phe Ala  
*lower case letters*

10

350 355 360

tgg aag cac cac gcc gag ctc ggt ccc atg atc aag cgc aag ttc tct 1273  
 Trp Lys His His Ala Glu Leu Gly Pro Met Ile Lys Arg Lys Phe Ser  
 365 370 375 380

15

gac cca gga gac gtc gag cgt gca cgc gag ttg gtc gag aaa agt gat 1321  
 Asp Pro Gly Asp Val Glu Arg Ala Arg Glu Leu Val Glu Lys Ser Asp  
 385 390 395

20

gga ttg gag aag acg aga gcc ttg gcg gag gag tat gcc cag aag gcg 1369  
 Gly Leu Glu Lys Thr Arg Ala Leu Ala Glu Glu Tyr Ala Gln Lys Ala  
 400 405 410

25

ttg gat gca att cgg acg ttc ccg gag agt cgc gca cgg aag ggt ttg 1417  
 ← Leu Asp Ala Ile Arg Thr Phe Pro Glu Ser Pro Ala Arg Lys Ala Leu  
 415 420 425

6

gag cag ttg acg gac aag gtg ttg act agg tca aga taggaattcgagct 1467  
 Glu Gln Leu Thr Asp Lys Val Leu Thr Arg Ser Arg  
 430 435 440

5

cggtaccggt ggatcctcta gagtcgacct gcaggcatgc aagcttggct gttttggcgg 1527  
 atgagagaag attttcagcc tgatacagat taaatcagaa cgcagaagcg gtctgataaa 1587

10

acagaatttg cctggcggca gtagcgcggt ggtccacact gaccccatgc cgaactcaga 1647

agtga

1653

15

<210> 2  
 <211> 440  
 <212> PRT

*delete*

20

<213> Saioella complicata  
 <400> 2  
 Met Ala Ser Pro Ala Leu Arg Ile Arg Ser Ile Ser Ser Arg Ser

*insert a space after each group of 10 bases*

*1653 see item 1 on Enr summary sheet*

15 1 5 10 misaligned  
Ile Ala Ser Leu Arg Ser Val Thr Leu Arg Thr Ala Ser Ala Pro  
20 25

30 25 Ser Leu Arg Leu Arg Cys Thr Pro Thr Ser Arg Pro Ser Ser Ser  
45 35 40

Trp Ala Ala Ala Val Ser Ser Ala Ser Arg Leu Val Glu Pro Asp  
50 55 60

Pro Asn Gln Pro Leu Ile Asn Pro Leu Asn Leu Val Gly Pro Glu  
65 70 75

5 Met Ser Asn Leu Thr Ser Asn Ile Arg Ser Leu Leu Gly Ser Gly  
80 85 90

His Pro Ser Leu Asp Thr Val Ala Lys Tyr Tyr Val Gln Ser Glu  
95 100 105

Gly Lys His Ile Arg Pro Leu Met Val Leu Leu Met Ala Gln Ala  
10 110 115 120

Thr Glu Val Ala Pro Lys Val Gln Gly Trp Glu Lys Val Val Glu  
125 130 135

Val Pro Val Asn Glu Gly Leu Ala Pro Pro Glu Val Leu Asn Asp  
140 145 150

15 Lys Asn Pro Asp Met Met Asn Met Arg Ser Gly Pro Leu Thr Lys  
155 160 165

Asp Gly Glu Ile Glu Gly Gln Thr Ser Asn Ile Leu Ala Ser Gln  
170 175 180

Arg Arg Leu Ala Glu Ile Thr Glu Met Ile His Ala Ala Ser Leu  
20 185 190 195

Leu His Asp Asp Val Ile Asp Ala Ser Glu Thr Arg Arg Asn Ala  
200 205 210

Pro Ser Gly Asn Gln Ala Phe Gly Asn Lys Met Ala Ile Leu Ala  
215 220 225

09/230,111

6

25 Gly Asp Phe Leu Leu Gly Arg Ala Ser Val Ala Leu Ala Arg Leu

230 235 240

Arg Asn Pro Glu Val Ile Glu Leu Leu Ala Thr Val Ile Ala Asn

245 250 255

Leu Val Glu Gly Glu Phe Met Gin Leu Lys Asn Thr Val Asp Asp

260 265 270

Ala Ile Glu Ala Thr Ala Thr Gin Glu Thr Phe Asp Tyr Tyr Leu

275 280 285

Gln Lys Thr Tyr Leu Lys Thr Ala Ser Leu Ile Ala Lys Ser Cys

290 295 300

Arg Ala Ser Ala Leu Leu Gly Gly Ala Thr Pro Glu Val Ala Asp

305 310 315

Ala Ala Tyr Ala Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gin Ile

320

325

← delete extra spaces

Val Asp Asp Met Leu Asp Tyr Thr Val Ser Ala Thr Asp Leu Gly

335 340 345

15 Lys Pro Ala Gly Ala Asp Leu Gin Leu Gly Leu Ala Thr Ala Pro

350 355 360

Ala Leu Phe Ala Trp Lys His His Ala Glu Leu Gly Pro Met Ile

365

← delete extra spaces

370

Lys Arg Lys Phe Ser Asp Pro Gly Asp Val Glu Arg Ala Arg Glu

380

385

390

Leu Val Glu Lys Ser Asp Gly Leu Glu Lys Thr Arg Ala Leu Ala

395

400

405

Glu Glu Tyr Ala Gln Lys Ala Leu Asp Ala Ile Arg Thr Phe Pro

410

415

420

25 Glu Ser Pro Ala Arg Lys Ala Leu Glu Gln Leu Thr Asp Lys Val

425 430 435

Leu Thr Arg Ser Arg

dashes not permitted  
invalid

440